OM protein - protein search, using sw model

GenCore version 5.1.3
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Run on: December 19, 2002, 14:59:27 ; Search time 22 Seconds
                                               (without alignments)
                                               2477.646 Million cell updates/sec

Title: US-08-813-323B-1
Perfect score: 2994
Sequence: 1 MESSKKMDAAGTLQPNPPLK.........IKDDTIFIKVIVDTSDLPDP 567

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR.73:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2994	100.0	567	2	I49272	CD40 receptor-asso
2	2886.5	96.4	568	2	A55960	CD40 receptor-asso
3	2718	90.8	543	2	S68467	CD40 receptor-asso
4	1189.5	39.7	557	2	JC6539	tumor necrosis fac
5	837.5	28.0	557	2	I61512	TNF receptor assoc
6	812.5	27.1	501	2	S56163	tumor necrosis fac
7	641.5	21.4	501	2	B55649	TNF-associated pr
8	640	21.4	416	2	A54750	TNF receptor assoc
9	556.5	18.6	409	2	I38026	MLN 62 protein-h
10	547	18.3	470	2	S71821	probable interleuk
11	523.5	17.5	522	2	T22238	hypothetical prote
12	209	7.0	509	2	A29361	DG17 protein - sli
13	164	5.5	458	2	B72765	hypothetical prote
14	161	5.5	919	2	I49642	estrogen-responsiv
15	157.5	5.3	634	2	S18199	myosin heavy chain
16	156.5	5.2	1039	2	T14265	golgin-245 - mouse
17	155.5	5.2	1218	2	A43906	nuclear phosphopro
18	155	5.2	609	2	E71410	probable centromer
19	152	5.1	1676	2	I53799	CGI protein - huma
20	151.5	5.1	1300	2	B96692	hypothetical prote
21	151.5	5.1	313	2	A48040	meprin A (EC 3.4.2
22	151	5.0	704	2	F96712	hypothetical prote
23	150	5.0	1085	2	S55696	myosin heavy chain
24	149	5.0	698	2	S32763	kinectin 1 - human
25	149	5.0	1356	2	T38077	hypothetical coile
26	147.5	4.9	1957	2	T13030	microtubule bindin
27	147.5	4.9	1690	2	S68950	laminin alpha-4 ch
28	146	4.9	1816	1	S68960	hypothetical prote
29	146	4.9	1679	2	S48335	hypothetical prote
30	145.5	4.9	1727	2	T50073	myosin-like coiled
31	145	4.8	944	2	S26710	spindle pole body
32	145	4.8	1005	2	A64465	hypothetical prote
33	144	4.8	1201	2	T08603	kinesin-related pr
34	143.5	4.8	1935	1	S06006	myosin beta heavy
35	142.5	4.8	764	2	I51302	myosin heavy chain
36	141.5	4.7	1940	1	A24922	myosin heavy chain
37	141.5	4.7	631	2	JC4298	hyaluronan recepto
38	141.5	4.7	1475	2	T33318	hypothetical prote
39	141.5	4.7	1935	1	A37102	myosin beta heavy
40	141	4.7	1940	2	A29320	myosin heavy chain
41	140.5	4.7	1957	2	A45627	conserved hypothet
42	140.5	4.7	1934	2	H69378	myosin heavy chain
43	140.5	4.7	886	2	I48153	myosin heavy chain
44	140	4.7	624	2	S28418	probable zinc-bind
45	140	4.7	879	2	C71083	conserved hypothet
	140	4.7	1313	2	A48467	myosin heavy chain

ALIGNMENTS

RESULT 1
I49272
CD40 receptor-associated factor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 18-Aug-2000
C;Accession: I49272
R;Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A;Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A;Reference number: I49272
A;Accession: I49272
A;Molecule type: mRNA
A;Residues: 1-567 <RES>
A;Cross-references: EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g719293
A;Genetics:
A;Gene: CRAF1
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Keywords: zinc finger
F;48-96/Domain: RING finger homology <RNG>

Query Match   100.0%; Score 2994; DB 2; Length 567;
Best Local Similarity   100.0%; Pred. No. 1e-165;
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MESSKKMDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKTVEDKKYKCEKCRLVLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MESSKKMDAAGTLQPNPPLKLQPDRGAGSVLVPEQGGYKEKFVKTVEDKKYKCEKCRLVLC 60

Qy   61 NPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVVCRNEG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQVVCRNEG 120

Qy   121 RGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RGCAEQLTLGHLLVHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK 180

Qy   181 SQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 SQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVF 240

Qy   241 QGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 QGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEIE 300

Qy   301 IERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 IERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRV 360

Qy   361 TELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWK 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIWK 420

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RESULT 2
A55960
CD40 receptor-associated factor 1 - human
N;Alternate names: CD40-binding protein
A;Residues: 1-568  <RES>
A;Molecule type: mRNA
A;Status: preliminary
A;Accession: A55960
A;Reference number: A55960; PMID:9518010; PMID:7533327
A;Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A;Residues: 1-128, 'M',130-568
C;Cross-references: GB:U15637; NID:g559910; PIDN:AAA56753.1; PID:g955911
A;Reference number: A55135; MUID:95073988; PMID:7527023
A;Accession: A55135
A;Status: nucleic acid sequence not shown
A;Residues: 1-128, 'M',130-568  <HUA>
A;Molecule type: mRNA
A;Cross-references: EMBL:L38509; NID:g693357; PIDN:AAA68195.1; PID:g695358
R;Sato, T.; Irie, S.; Reed, J.C.
A;Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.
J. Biol. Chem. 269, 30069-30072, 1994
R;Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
A;Cross-references: EMBL:U21092; NID:g726087; PIDN:AAC50112.1; PID:g726088
A;Residues: 1-568  <MOS>
A;Molecule type: mRNA
A;Status: nucleic acid sequence not shown
A;Accession: A55649
A;Reference number: A55649; MUID:95163092; PMID:7859281
A;Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins fo
A;Reference number: A55960; A55649; A55135
R;Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 01-Dec-2000
C;Accession: A55960; A55649; A55135
C;Species: Homo sapiens (man)
C;Cross-references: EMBL:U21092; NID:g726087; PIDN:AAC50112.1; PID:g726088
R;Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995

Query Match             96.4%;  Score 2886.5;  DB 2;  Length 568;
Best Local Similarity   96.1%;
Matches  546;  Conservative    7;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 MESSKKMDAAGTLQPNPPLKLQPDRGAGS-VLVPEQGGYKEKFVKITVEDKYKCEKCRLVL 59
              |||||||  ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKIVEDKYKCHLVL    60

Qy         60 CNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQYVCRNE 119
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE 120

Qy        120 GRGCAEQLTLGHLLVHLKNEQFEELPCLRADCKEKVLRKDHVEKACKYREATCSHC   179
              |||||||||||||||||||||:  ||||||||||||||||||||||||||||||||
Db        121 SRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC 180

Qy        180 KSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV 240
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RESULT 3
S68467
CD40 receptor-associated protein CAP-1 - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 08-Dec-2000
C;Accession: S68467; I53498
C;Cross-references: EMBL:L38509; NID:g693357; PIDN:AAA68195.1; PID:g695358
R;Sato, T.; Irie, S.; Reed, J.C.
FEBS Lett. 358, 113-118, 1995
A;Title: A novel member of the TRAF family of putative signal transducing proteins bi
A;Reference number: 153498; MUID:95129692; PMID:7530216
A;Accession: S68467
A;Residues: 1-543  <SAT>
A;Molecule type: mRNA
A;Status: nucleic acid sequence not shown
A;Gene: CAP-1
C;Genetics:
A;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Superfamily: homodimer; signal transduction; zinc finger
C;Keywords: signal transduction; zinc finger
F;49-97/Domain: RING finger homology <RNG>

Query Match             90.8%;  Score 2718;  DB 2;  Length 543;
Best Local Similarity   91.5%;
Matches  520;  Conservative    7;  Mismatches   15;  Indels   26;  Gaps    2;

Qy          1 MESSKKMDAAGTLQPNPPLKLQPDRGAGS-VLVPEQGGYKEKFVKITVEDKYKCEKCRLVL 59
              |||||||  ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 MESSKKMDSPGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFVKIVEDKYKCHLVL    60

Qy         60 CNPKQTECGHRFCESCMAALLSSSSPKCTACQESIIKDKVFKDNCCKREILALQYVCRNE 119
              |||||||||||||||||||||||||||||||:||||||||||||||||||||||||| ||
Db         61 CSPKQTECGHRFCESCMAALLSSSSPKCTACQESIVKDKVFKDNCCKREILALQIYCRNE 120

Qy        120 GRGCAEQLTLGHLLVHLKNEQFEELPCLRADCKEKVLRKDHVEKACKYREATCSHC   179
              |||||||||||||||||||||:  ||||||||||||||||||||||||||||||||
Db        121 SRGCAEQLTLGHLLVHLKNDCHFEELPCVRPDCKEKVLRKDLRDHVEKACKYREATCSHC 180

Qy        180 KSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV 239
              ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCV 240

Qy        240 FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI 300

Qy        300 EIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR 360
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                                                                         (Result 2, continued)
Qy        240 EIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR 359
Db        241 FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSLHNQICSFEI 300

Qy        300 EIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR 359
Db        301 EIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNR 360

Qy        360 VTELESVDKSAGQAAARNTGLLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIW 419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VTELESVDKSAGQVARNTGLLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIW 420

Qy        420 KIRDYKRRKQEAVMGKTLSLIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFVIMRG 479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 KIRDYKRRKQEAVMGKTLSLIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFVIMRG 480

Qy        480 EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQ 540

Qy        540 TVLENGTYIKDDTIFIKVIVDTSDLPDP 567
              |||||||||||||||||||||||||||
Db        541 TVLENGTYIKDDTIFIKVIVDTSDLPDP 568
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                                                                         (Result 1, continued — top)
Qy        421 IRDYKRRKQEAVMGKTLSLSIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFVIMRGE 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IRDYKRRKQEAVMGKTLSLSIYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFVIMRGE 480

Qy        481 YDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 YDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQT 540

Qy        541 VLENGTYIKDDTIFIKVIVDTSDLPDP 567
              |||||||||||||||||||||||||||
Db        541 VLENGTYIKDDTIFIKVIVDTSDLPDP 567
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Db  276  EIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRSFRQNWEEADSMKSSVESLQNR  335
          ||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Qy  360  VTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETASYNGVLIW  419
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db  336  VTELESVDKSAGQVARNTGLLESQLSRHDQMLSVHDIRLADMDLRFQVLETASYNGVLIW  395

Qy  420  KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG  479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  396  KIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRG  455

Qy  480  EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDDPNSSSFKKPTGEMNIASGCPVFVAQ  539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  456  EYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDDPNSSSFKKPTGEMNIASGCPVFVAQ  515

Qy  540  TVLENGTYIKDDTIFIKVIVDTSDLPDP  567
          ||||||||||||||||||||||||||||
Db  516  TVLENGTYIKDDTIFIKVIVDTSDLPDP  543
```

RESULT 4
JC6539
tumor necrosis factor receptor-associated factor 5 homolog - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 18-Aug-2000
C;Accession: JC6539
R;Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.; Yam...
Gene 207, 135-140, 1998
A;Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr...
A;Reference number: JC6539; MUID:9817274S; PMID:9511754
A;Accession: JC6539
A;Molecule type: mRNA
A;Residues: 1-557 <MIZ>
A;Cross-references: DDBJ:AB000509; NID:g2982670; PIDN:BAA25262.1; PID:g2982671
A;Comment: This protein is involved in transduction of signals from various tumor necros...
mphotoxin-beta receptor.
C;Genetics:
A;Map position: 1q32.3-1q41.1
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Keywords: coiled coil; tumor; zinc finger
F;41-90/Domain: RING finger homology <RRN>

Query Match   39.7%; Score 1189.5; DB 2; Length 557;
Best Local Similarity 43.4%;   Pred. No. 1.8e-61;
Matches 232;   Conservative 112;   Mismatches 170;   Indels 21;   Gaps 9;

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Qy   41  KFVKTVEDKYKCEKCRLVLCNPKQ?ECGHRFCESCMAALLS-SSSPKCTACQESIIKDKV   99
          ||| ::|: |||:|:|| |:||: |:||||||| :| ||||  :::||||| |||:|:||
Db   34  QFVERLEERYKCAFCHSVLHNPHQTGCGHRFCQHCILSLRELNTVPICPVDKVIKSQEV   93

Qy  100  FKDNCCKREILALQVYCRNEGRGCAEQLTLGHLLVHLKNEGCQFEELPCLRADCKEKVLRK  159
          ||||||||||||||||| ||:|:||  |||||||:|:|::|| ||||||| |:||::|:||
Db   94  FKDNCCKREVLNLYVCSN-APGCNAKVILGRYQDHLQ-QCLFQPVQCSNEKCREPVLRK  151

Qy  160  DLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSA  219
          |||||||||||||||||||| ||| ||:|:|||||||||||||||||||||:||:|||:|
Db  152  DLKEHLSASCGFRKEKCLYCKKDVVVINLQNHEENLCPEYPVFCPNNCA-KIILKTEVDE  210

Qy  220  HLSECVNAPSTCSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNE  279
          |||:|||||||||:|||||| |||||:|:|||:||| ||||||:|||:::|:| :|:|:
Db  211  HLAVCPEAEQQCPFKHYGCAVTDKRRNLQOHEHSALREHRRLVLEKNVQLEEQISDLHKS  270

Qy  280  SVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPF  339
          :::::| :|:|:||||::|:|:||||||||||||||||||||||||||||||||||||||
Db  271  LEQESKIQQLAETIKKLEKEFQFAQLFGKNGSFLPNIQ-VFASHIDKSAWLEAQVHQL  329

Qy  340  -----RQNMEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSV  393
               :::|:: :|:| ||:|||||||||||||| ||||||||||||||||||||||||
Db  330  LQMVNQQQNFDLRPLMEAVDTVKQKITLLENND------QRLAVLEEETNKHDTHINI  382

Qy  394  HDIRLADMDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKM  453
          |: :|:  ::| :| ||:|||| ||||| |:| ::|||| |||::||:|| |:|:|||||
Db  383  HKAQLSKNEERFKLLEGTCYNGKLIWKVTDYKMKREAVDGHTVSIFSQSFYTSRCGYRL  442
```

RESULT 5
I61512
TNF receptor associated factor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: I61512
R;Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A;Title: A novel family of putative signal transducers associated with the cytoplasm1...
A;Reference number: A54750; MUID:94349371; PMID:8069916
A;Accession: I61512
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-501 <RES>
A;Cross-references: GB:L35303; NID:g532620; PIDN:AAC37662.1; PID:g532621
C;Genetics:
A;Gene: TRAF2
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Keywords: zinc
F;30-78/Domain: RING finger homology <RNG>

Query Match   28.0%; Score 837.5; DB 2; Length 501;
Best Local Similarity 33.5%;   Pred. No. 3.4e-41;
Matches 194;   Conservative 88;   Mismatches 198;   Indels 99;   Gaps 16;

```
Qy    7  MDAAGTLQPNPPLKILQPDRGAGSVLVPEQGGYKERFVKT-VEDKYKCEKCRLVLCNPKQT   65
          ||||:||||    |:||||          ||:|||:|||:  ::|||||||| ||| || |
Db    1  MAAASVTSPGSLELLQP----------GFSKILLGTRLEAKYLCSACKNILRPFQA   47

Qy   66  ECGHRFCESCMAALLSSSSPKCTAC-----QESII--KDKVRKDNCCKREILALQVYC  116
          :|||| | |||:| | :::|:|:||     |:||:  ||||::|:|||||||||:||||
Db   48  QCGHRYCSFCLTSILSLSGPQNCAACVYEGLYEEGISILESSSAFFDNAARREVESLPAVC  107

Qy  117  RNEGRGCAEQLTLGHLLVHLKNEGCQFEELPCLRADCKEKYLRKDLRDHVEKACKYREATC  176
          :||:|||  ||||||||:|||:|:| ||||||| |:||::|||:|||||||||||||||:|
Db  108  PND--GCTWKGTLKEYESCHEGLCPFLLTEC--PACKGLVRLSEKEHHTEQECPKRSLSC  163

Qy  177  SHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRY  236
          :||:: | :::|::||||:|||:: | |:|| :: |:: :|::|:||||||||||||||
Db  164  QHCRAPCSHVDLEVHYEV-CPKFPLTC-DGCGKKKIPRETFQDHVRACSKCRVLCRFHTV  221

Qy  237  GCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVS------------LLQNESVEKNKS  286
          ||| |:|::: :||| |||:|||||||||||:| :||:            ||||||:|:|
Db  222  GCSEMVETENLQDHELQRLREHLALL---LSSFLEAQASPGTLNQVGPELLQRCQILEQK-  278

Qy  287  IQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQNWEEA  346
          | :: |::| |:::  :|                         :|:   :|:
Db  279  IATFENIVCVLNREVER-------------VAVTAEACSRQHRLDQD----------  312

Qy  347  DSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQ  406
          :|::||||::|:|:                            :|:|:||||| :|::: :|
Db  313  -----KIEALSNKVQQLE--------------RSIGLKDLAMADLEQKVS  343

Qy  407  VLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGK  466
          .|| : |:||:|||| |: :|||||:|: ||:|:|: |||:||||||||||||||||:|:
Db  344  ELEVSTYDGVFIWKISDFTRKRQEAVAGRTPAIESPAFTYSRIGYKMCLRVYLNGDGTGR  403

Qy  467  GTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDDPNSSSFKKPTGE  526
          |||||||||:|:| ||||| ||| |||||||:|: ||| | |||:||| :||||| || :
Db  404  GTHLSLFFVVMKGPNDALLQWPFNQKVTLMLLDH-NNREHVIDAFRPDVTSSSFQRPVSD  462

Qy  527  MNIASGCPVFVAQTVLE-NGTYIKDDTIFIKVIVDTSDL  564
          :|||||||:||||||| | :||||||||||||||||||
```

```
Qy  454  CARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKP  513
          ||| |||||| |:| :||| :|:::|||: |||| || |:||||||:| |:::: :| ||
Db  443  CARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWPFRQRVTLMLLDQ-SGKKNIMETFKP  501

Qy  514  DPNSSSFKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTSDLPD  566
          |||||||| | ||||||||||:|||: |||   |:||||||:|:|||.|| :|:|
Db  502  DPNSSSFKRPDGEMNIASGCPRFVAHSVLENAKNAYIKDDTLFLKVAVDLIDLED  556
```

Db   463 MNIASGCPLFCPVSKMEAKNSIYVRDDAIFIKAIVDLTGL 501

RESULT 6
S56163
tumor necrosis factor type 2 receptor associated protein - human
N;Alternate names: TNF receptor-associated protein
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change 03-Nov-2000
C;Accession: S56163; S58925; S58926; I38729
R;Song, H.Y.; Donner, D.B.
Biochem. J. 309, 825-829, 1995
A;Title: Association of a RING finger protein with the cytoplasmic domain of the human t
A;Reference number: S56163; MUID:95366958; PMID:7639698
A;Molecule type: mRNA
A;Accession: S56163 <SON>
A;Residues: 1-501 <SON1>
A;Cross-references: EMBL:U12597; NID:g975272
R;Song, H.Y.; Donner, D.
A;Molecule type: mRNA
A;Reference number:
submitted to the EMBL Data Library, July 1994
A;Description: Association of a RING finger protein with the cytoplasmic domain of the h
A;Accession: S58925
A;Molecule type: mRNA
A;Residues: 1-42, 63-342, 363-501 <SON2>
A;Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273
A;Accession: S58926
A;Molecule type: mRNA
A;Residues: 1-42, 63-342, 363-501 <SON3>
A;Cross-references: EMBL:U12597; NID:g975272
A;Title: A novel family of putative signal transducers associated with the cytoplasmic d
A;Reference number: I38729
A;Accession: I38729
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-342, 'RPFQAOCGHRYCSFCLASIL',363-501 <ROT>
A;Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273
C;Genetics:
C;Gene: GDB:TRAF2; TRAP
C;Cross-references: GDB:6268629; OMIM:601895
A;Map position: 9q34-9q34
A;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Keywords: zinc finger
F;30-78/Domain: RING finger homology <RNG>

Query Match   27.1%; Score 812.5; DB 2; Length 501;
Best Local Similarity   33.7%; Pred. No. 9.6e-40;
Matches 197; Conservative 92; Mismatches 185; Indels 111; Gaps 21;

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Qy    7 MDAAGTLQPNPPLKLQDPDRGAGSVLVPEQGGVKEKFVKT-VEDKYKGEKCRLVLCNPKQT  65
Db    1 ----MAAASVTPPGSLELLQP----------GFSKTLLGTKLEAKYLCSACRNVLRRPFQA  47

Qy   66 ECGHRFCESCMAALLSSSSPKCTAC-QESIIKDKV------------FKDNCCKREIIALQYC 116
Db   48 QCGHRYCSFCLASILSSSGPQNCAACVHEGIYEEGISILESSSAFPDNAARREVSLPAVC  107

Qy  117 RNEGRGCAEQLILGHLLVHLKNECQFEELPCLRAD-----CKEKVLRKDLRDHVEKACKYRE 173
Db  108 PSD--GCTWKGTLKEY-----ESCHEGRCPLMLTECPACKGLVRLGEKERHLEHECPERS  160

Qy  174 ATCSHCKSQVPMIKLQKHEDTDCPCVVWSCPHKCSVQTLLRSELSAHLSECVNAPSTCSF  233
Db  161 LSCRHCRAPCGADVKAHHEV-CPKFFLTC-DGCGKKKIPREKFQDHVKTCGKCRVPCRF  218

Qy  234 KRYGCV--FQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKK-------------VSLLQN-ES 280
Db  219 HAIGCLETVEGEKQQ--EHEVQWLREHLAML-LSSVLEAKPLIGDQSHAGSELLQRCES  274

Qy  281 VEKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILIHLQRVIDSQOAEKLKELDKEIRPER 340
Db  275 LEKKLTA--TFENIVCVLNREVER---------------------------VAMTAEACS------R 305

Qy  341 QNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLAD  400
Db  306 QHRLDQD----KIEALSSKVQOLE------------------------------RSIGLKDLAMAD 337

Qy  401 MDLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMGARVIN  460
Db  338 LEQKVLEMEASTYDGVFIWKISDFPRKLQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLN 397

Qy  461 GDGMGKGTHLSLFFVIMRGEYDALLLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDDPNSSF 520
Db  398 GDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQ-NNREHVIDAFRPDVTSSSF  456

Qy  521 KKPTGEMNIASGCPVFVAQOIVLE-NGTYIKDDTIFIKVIVDTSDL 564
Db  457 QRPVNDMNIASGCPLFCPVSKMEAKNSIYVRDDAIFIKAIVDLTGL 501
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RESULT 7
B55649
TNFR-associated protein EB16 - human
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 08-Oct-1999
C;Accession: B55649
R;Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995
A;Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins
A;Reference number: A55649; MUID:95163092; PMID:7859281
A;Status: preliminary
A;Accession: B55649
A;Molecule type: mRNA
A;Residues: 1-416 <MOS>
A;Cross-references: GB:U19261; NID:g675461; PIDN:AAA62309.1; PID:g675462

Query Match   21.4%; Score 641.5; DB 2; Length 416;
Best Local Similarity   35.5%; Pred. No. 5.8e-30;
Matches 165; Conservative 71; Mismatches 126; Indels 103; Gaps 17;

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Qy  137 KNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDC  196
Db   15 ENEFPPGCPPTVCQDPKEP------------------------RALCCAGCLSENP----RNGEDQIC 54

Qy  197 PCVVWSCPHKCSVQTL--------LRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIK  248
Db   55 P----------KCRGEDLQSISPGSRLRTQEKAH-PEVAEAGIGCFFAGVGCSFKGSPQSVQ 105

Qy  249 AHEASSAVQHVNLL----KEWS-----------NSLEKKVSLLQ-NESVERNKSIQ-SLH  291
Db  106 EHEVTSQTSHLNLLLGFMKQWRARLGGGLESGPMALEQNLSDLQLQAAVEVAGDLEVDCY 165

Qy  292 NQICSFEIEIEROKEMLRNNESKILIHLQRVIDSQAEKLKELDKEIRPFRQNWEEADSMKS 351
Db  166 RAPCS-------ESQEE---------LALQHFM--KEKLLAELEGKLRVF-----------E 198

Qy  352 SVESLQNRVTELESVDKSAGQAARNTGLLESQLSRH----------DQTLSVDIRIA  399
Db  199 NIVAVLNKEVE-----ASHLALATSIHQSOLDRERILSLEQRVVELQQTLAQKDQALG 251

Qy  400 DMDLRFQVLETASYNGVLVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVL 459
Db  252 KLEQSLRILMEEASFDGTFLWKITNVIRCHESACGRTVSLFSPAFVTAKYGYKLCIRLYL 311

Qy  460 NGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDDNSSS  519
Db  312 NGDGTGKRTHLSLFFIVIMRGEYDALLPWPFRNKVTFMLLDQ-NNREHAIDAFRPDLSSAS 370

Qy  520 FKKPTGEMNIASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTS 562
Db  371 FQRPQSEfNVASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVETS 415
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RESULT 8

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A54750
TNF receptor associated factor 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: A54750
R;Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A;Title: A novel family of putative signal transducers associated with the cytoplasmic d
A;Reference number: A54750; MUID:94349371; PMID:8069916
A;Accession: A54750
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-409 <RES>
A;Cross-references: GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619
C;Genetics:
A;Gene: TRAF1

Query Match          21.4%;  Score 640;  DB 2;  Length 409;
Best Local Similarity 35.5%;  Pred. No. 7e-30;
Matches  162;  Conservative   72;  Mismatches 136;  Indels   86;  Gaps  15;

Qy  137 KNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDC 196
            ||||| ||                          :|||  |||  |||||||
Db    9 ENEFQF---GCPPAPCQD--------------------PSEPRVLCCTACLSE----NLRDDEDRIC 48

Qy  197 PCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSPFKRYGCVFQGTNQQIKAHEASSAV 256
            |||  ||| |   ||  :|||   | ||||| ||||||||||| || |||||||||||||
Db   49 PKCRADNLHPVSPGSPLTQE-KVH-SDVAEAIMCPFAGVGCSFKGSPQSMQEHEATSQS 106

Qy  257 QHVNL----LKEWSNS------------------LEKKVSLLQNESVEKNKSIQSLHNQICSFEIEI 301
                 |||  ||                      |  | | | |||   ||   |||  |  ||
Db  107 SHLYLLAVLKEKKSSPGSNLGSAPMALERNLSELQ---------------LQAAVEATGDLEVDC 157

Qy  302 EROKEMLRNNESKILHLQRVIDSQAEK-LKELDKEIRPFRQNWEEADSMKSVVESLQNRV 360
            || | | |||  || ||||:|    |    |||  |       ::||:||  ||||  |
Db  158 YRAPCCESQQEELALQHLVK-------EKLLAQLEEKLRVF---------------ANIVAVLNKE 200

Qy  361 TELESVDKSAGQAARNTGLLESQLSRH--------------DQTLSVHDIRLADMDLRFQVL 408
            |  | ||  |      || :| ||                : | || | |  |  |  ||
Db  201 VE------ASHLALAASIHQSOLDREHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLM 253

Qy  409 ETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGT 468
            |:|  || |  |:  |  ||  |      |||  | |    | ||  ||  |  | :  |
Db  254 EEASFDGTFLWKITNVIKRCHESVCGRRVSLFSPAFVTAKYGYKLCLRLYILNGDGSGKKT 313

Qy  469 HLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSEFKKPTGEMN 528
            |||| |:  |    |||||||| ||||||||  ||||| |||| |||    |  |  |  |
Db  314 HLSLFIVIMRGEYDALLPWPFRNKVTFMLLDQ-NNREHAIDAFRPDLSSASFQRPQSETN 372

Qy  529 IASGCPVFVAQTVLEN--GTYIKDDTIFIKVIVDTS 562
            :||| | |||  :||    |:|||||||||||||
Db  373 VASGCPLFFPLSKLQSPKHAYVKDDTMFLKCIVDTS 408


RESULT 9
I38026
MLN 62 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 02-Sep-2000
C;Accession: I38026; S60681
R;Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.
Genomics 28, 367-376, 1995
A;Title: Identification of four novel human genes amplified and overexpressed in breast
A;Reference number: I37080; MUID:96095245; PMID:7490069
A;Accession: I38026
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-470 <RES>
A;Cross-references: EMBL:X80200; NID:g951276; PIDN:CAA56491.1; PID:g951277
C;Genetics:
A;Gene: MLN62; CART1
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology


F;14-63/Domain: RING finger homology <RRN>

Query Match          18.6%;  Score 556.5;  DB 2;  Length 470;
Best Local Similarity 24.1%;  Pred. No. 5.5e-25;
Matches  142;  Conservative   80;  Mismatches 174;  Indels  193;  Gaps  12;

Qy   37 GYKEKFVKTVVEDKYKCEKCRLVLCNPKQ-TECGHRFCESCMAAILSSSSSPKCTACQESII 95
            ||||  :| |          |  |        |||  | :  |:  ||    |   |  |
Db    3 GFDYKFLEKPKRRLLCPLCGKPMREPVQVSTCGHRFCDTCLQEFLSEGVFKCPEDQLPLD 62

Qy   96 KDKVFKDNCCKREILALQVYCRNEGRGCAEQLTIGHLLVHLKNECQFEELPC------- 147
            :  |     |   | |  ||         | | |  |  ||:||| |||| ||
Db   63 YAKIYPDPELEVQVLGLPIRCIHSEEGCRWSGPLRHLQGHL-NTCSFNVIPCPNRCPMKL 121

Qy  148 ----------LRADCKE------------------------KVLRKDLR 162
Db  122 SRRDLPAHLQHDCPKRLRLKCEECGCDFSGEAYESHEGMCPQESVYCENKCGARMMRGLLA 181

Qy  163 DHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLS 222
            ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  182 QHATSECPKRTQPCTYCTKEFVPDTIQSHQ-YQCPRLPVACPNQCGVGTVAREDLPGHLK 240

Qy  223 E-CVNAPSTCSPFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESV 281
            | ||  ||||||||||||||||||||||||||||||        || |  ||  | |||||
Db  241 DSCNTALVLICPFKDSGCGCKHRCPKLAMARHVEESVKPHLAMM--------------- 281

Qy  282 EKNKSIQSLHNQICSFEIEIEROKEMLRNNESKILHLQRVIDSQAEKLKELDKEIRPFRQ 341
                           ||  | |        || | | |||  ||||||:|
Db  282 ----------------CA--------------LVSRQRQELQELRREL------------ 299

Qy  342 NWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADM 401
Db  300 ---------------------------------------EELSV----------------- 304

Qy  402 DLRFQVLETASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNG 461
            :  | |  |:||||||||||||||||||||||||||  |||||||||||||||||||||
Db  305 -------GSDGVLIWKIGSYGRRLQEAKAKPNLECFSPAFYTHKYGYKLQVSAFLNG 354

Qy  462 DGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQG----SSRRHLGDAFKPDPNS 517
            ||:||||||||| | ||||||||||||| |||  | |||      |||||||||| |||
Db  355 NGSGEGTHLSLIVIRVLPGAFDNLLEWPFARRVTFSLLDQSDPGLAKPQHVTETFHPDPNW 414

Qy  518 SSEFKKP------TGEMNIASGCPVFVAQTVLENGTYIIKDDTIFIKVIVD 560
            |  |        | |:| | | | || |  :||  |:||||||||||||:|
Db  415 KNFQKPGTWRGSLDESSLGFGYPKFISHQDIRKRNYVRDDAVFIRAAVE 463


RESULT 10
S71821
probable interleukin 1 signal-transducing protein TRAF6 - human
C;Species: Homo sapiens (man)
A;Title: TRAF6 is a signal transducer for interleukin-1.
A;Reference number: S71821; MUID:96434892; PMID:8837778
C;Accession: S71821
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Sep-2000
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-522 <CAO>
R;Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.
Nature 383, 443-446, 1996
R;Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.
submitted to the EMBL Data Library, October 1996
A;Cross-references: EMBL:U78798; NID:g1734245; PIDN:AAB38751.1; PID:g1732425
A;Accession: S78550
A;Molecule type: mRNA
A;Residues: 1-275, 'A', 277-522 <CAW>
A;Cross-references: EMBL:U78798; NID:g1724425; PIDN:AAB38751.1; PID:g1732426
C;Genetics:
A;Gene: TRAF6
C;Function:
A;Description: activates transcription factor NF-kappa-B in response to interleukin-1
```

```
A;Note: interleukin-1 induces the association of protein of TRAF6 with the IRAK serine/threonine ki
t
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C;Keywords: signal transduction; zinc finger
F;66-114/Domain: RING finger homology <RRN>

Query Match       18.3%;   Score 547;   DB 2;   Length 522;
Best Local Similarity  26.6%;   Pred. No. 2.2e-24;
Matches 144;  Conservative 101;  Mismatches 201;  Indels 96;  Gaps 16;

Qy   29  SVLVPEGGYKEKFVKTVEDKYKCCKCRLVLCNPKQTEGHRFCESCMAALLSSSSPKCT    88
Db   47  SSFMEELQGVDVEFDDPPLESKVECPICLMALREAVQTPCGHRFCRACIIKSIRDAGHKCP 106

Qy   89  ACQESIIKDKVFKDNCCKREILALQVYCRNEGRGCAEQLTIGHLLVHLKNECQFEELPCL  148
Db  107  VDNEILLENQLPPDNFAKREILSLMVACPNE--GCLHKMELRHLEDH-QAHCEFALMDC-  162

Qy  149  RADCKEKVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCS  208
Db  163  -PQCQRPQKFHINIHLLKDCPRRQVSCDNCAASMAFEDKEIH-DQNCPLANVICEY-CN   219

Qy  209  VQTLLRSELSAHLS-ECVNAPSTCSFKRYGGCVFQGTNQQIKAHEASSAVQHVNLLKEWSN 267
Db  220  T-ILIREQMPNIHYDLDCPTAIPCTETSTFGGCHEKMQRNHLARHLQENTQSHMRMLAQPVH 278

Qy  268  SLEKKVSLLQNESVEKNKSIQSLHNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAE  327
Db  279  SL-----SVIPDSGYIS--EVRNFQETIHQLEGRLVRQDHQIRELTAKMETQSM        325

Qy  328  KLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRH  387
Db  326  YVSELKRTIR------------TLEDKVAEIEA------                        346

Qy  388  DQTLSVHDIRLADMDLRFQVLETASYNGVLITWKIRDY----KRRKQEAVMGKTLSLYSQP 443
Db  347  ------QQCNGIYIWKIGNFGMHLKCQQEEE----KPVVIHSPG                  379

Qy  444  FYTGYFGYKMCARVYLN-GDGMGKGTHLSLFFVIMRGEYDALLPWPFPKQKVTLMLMDQGS 502
Db  380  FYTGKPGYKLCMRLHLQLPTAQRCANYISLFVHTMQGEYDSHLPWPFQGITRLTILDQSE  439

Qy  503  S--RRHLGDAFKPDPNSSSFRKPTGEMNIAS-GCPVFVAQTVLENGTYIKDDTIFIKVIV  559
Db  440  APVRQNHEEIMDAKPELLAFQRPTIPRNPKGFPGYVTFMHLEALRQRTFIKDDTLLVRCEV 499

Qy  560  DT  561
Db  500  ST  501
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RESULT 11

T22238

hypothetical protein F45G2.6 - Caenorhabditis elegans

```
C;Species: Caenorhabditis elegans
A;Reference number: Z19535
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T22238
A;Status: preliminary; translated from GB/EMBL/DDBJ
R.Lindsay, S.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19535
A;Molecule type: DNA
A;Residues: 1-509 <WIL>
A;Accession: T22238
A;Cross-references: EMBL:Z93382; PIDN:CAB07615.1; GSPDB:GN00021; CESP:F45G2.6
A;Experimental source: clone F45G2
A;Genetics:
A;Gene: CESP:F45G2.6
A;Map position: 3
A;Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 360/1; 395/3; 448/3
C;Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
F;61-107/Domain: RING finger homology <RRN>
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Query Match       17.5%;   Score 523.5;   DB 2;   Length 509;
Best Local Similarity  26.2%;   Pred. No. 4.8e-23;
Matches 137;  Conservative 68;  Mismatches 188;  Indels 129;  Gaps 12;

Qy   52  CEKCRLVLCNPKQTEGHRFCESCMAALLSSSSPKCTACQQESIIKDKVFKDNCCKREILA 111
Db   65  CPICEQALRDPIKLNCGHHYCRQCFEN--ENRTPGCAACQTIIQPELCQHDRAKQQILA   122

Qy  112  LQVYCRNEGRGCAEQLTIGHLLVHLKNECQFEEL-ELPCLRADCKEKVLRKDLRDHVEKACK 171
Db  123  LPVVCTPFESSGCPWDSGQLGTLHDHL-SECTFKSSLKCEK--CGRQFAKNDLEKHRAK-CE 178

Qy  171  YREATCSHCKSQVPMIKLQKHEDTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPST  230
Db  179  LNRAVCSFCNKTIRDSDRERIPKT-CPQVIISCPFQCGLITDRPRLEIEAHCPSCPNVDNV 237

Qy  231  CSFKRYGCVFQGTNQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQNESVEKNKSIQSL  290
Db  238  CPFVPYGCTFAGGKESIQOHLSDEPVRHLMYLCDEITDLKGTYELM--              283

Qy  291  HNQICSFEIEIERQKEMLRNNESKILHLQRVIDSQAQEKLKELDKEIRPFRQNWEEADSMK 350
Db  284  ---ERDMGSFNDRQTRIL--                                          307

Qy  351  SSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLET  410
Db  308  --FGPQLIWKIDKLQQRTNEAKSGADTIFSVPFMSHRFGYKMMACACLFGDGSSAGKSI   365

Qy  411  ASYNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHL  470
Db  366  SLYVLLKGEFDPTLEWPFHRAIKISLLDQNPREDRVNITVYIDPRKLKANEKFLARPR    425

Qy  471  SLFFVIMRGEYDALLPWPFPKQKVTLMLMDQGS-----SRRHLGDAFKPDPNSSSFKKPT  524
Db  426  GERNAAPGSQSFCSLAILQN--YVKDKIVQDIDVDRCETLP                     465

Qy  525  GEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVIDTSD-LP  565
```

RESULT 12

A29361

DG17 protein - slime mold (Dictyostelium discoideum)

```
C;Species: Dictyostelium discoideum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 29-Oct-1999
C;Accession: A29361
R;Driscoll, D.M.; Williams, J.G.
Mol. Cell. Biol. 7, 4482-4489, 1987
A;Title: Two divergently transcribed genes of Dictyostelium discoideum are cyclic AMP
A;Reference number: A29361; MUID:88142840; PMID:2830496
A;Accession: A29361
A;Molecule type: DNA
A;Residues: 1-458 <DRI>
A;Cross-references: GB:M18106; NID:g167729; PIDN:AAA33192.1; PID:g167730
A;Accession: A29361
C;Keywords: DNA binding; zinc finger
```

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Query Match       7.0%;   Score 209;   DB 2;   Length 458;
Best Local Similarity  20.3%;   Pred. No. 6.3e-05;
Matches 115;  Conservative 80;  Mismatches 177;  Indels 194;  Gaps 27;

Qy   47  EDKYKCEKCRLVLCNPKQTEC--GHRFCESCMAALLSSSSPKCTACQ------ESI     94
Db   22  KNKYTCPICFEFIYKKQIYQCKSGHHACKECWEKSLETKR-ECMCKSVVNSYNDLSRCL   80

Qy   95  IKDKVF--KDNCC-----KREILALQVYC----------RNEGRGCAEQLTIGHLL     133
Db   81  MVERAFDKKECCIYSFNEQIVEGGTNCSPPDGASVQNQRNLIKDEENGCKEIEVDQID   140

Qy  134  VHLKNECQFEELPCLRADCKEKVLRKDLRDHVEKACKYREATCSHCK-SQVPMIKLQKHE 192
Db  141  SHLIN-CQYKFVTCSFKGC-EKILR--MNSIKMNGGFKLVTCDFCKRDDIKKKELETHY  195
```

```
Qy  193 DTDCPCVVVSCPHKCSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGTNQOIKAHEA 252
Db  196 KT-CPMVPIDCSQGCGSVKIERKSIIDHIENDCCNTQIPCKYFBQGC------------ 240

Qy  253 SSAVQHVNLLKEWSNSLEKKVSLLQONESVEKNKSIQSLHNQICSFEIEIEROKEMLRNNE 312
Db  241 ----------KVEMKRSELQN--------------------------------------- 251

Qy  313 SKILHLQRVIDSQOAEKLKELDKEIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQ 372
Db  252 ----HLERV---------------NHQNY-----MGILIEKLLNQV-----------GQ 275

Qy  373 AARNTGLLESQLSRHDQTLSVHDIRLADMDLRFQVLETA--SYNGVL-IWKIRDY----- 424
Db  276 SKKT-----HDELLKIEDLSLLVIKFSDACLKKQVLPKALDICSNGYRNKWIISNYSSVA 331

Qy  425 -KRRKQEAVMGKTLSLYSQPPYTGYFGYKMCARVYLNGDMGKGTHLSLFFVI------- 476
Db  332 KSKLNCQALSSPMSILSHLF-----QVC--VTPKGD-ENKEYISLYLRVNNIEEPN 380

Qy  477 -MRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFFKKPTGEMNIASGCPV 535
Db  381 SLKVEYSFTL----------VNVLDKSKSTRKKED------------------------- 420

Qy  536 FVAQTVL--ENGTYIKDDTIFIKVIV 559
Db  421 FLISDLINKENGWLSNDDKLIIEIYI 446
```

RESULT 13
B72765
hypothetical protein APE0110 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001
C;Accession: B72765
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72765
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-919 <KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79020.1; PID:g5103499
C;Experimental source: strain K1
C;Genetics:
A;Gene: APE0110

Query Match   5.5%; Score 164; DB 2; Length 919;
Best Local Similarity 21.1%; Pred. No. 0.057;
Matches 98; Conservative 77; Mismatches 176; Indels 114; Gaps 16;

```
Qy   25 RGAGSVLVPEQGGYKEKFVKTVEDKYKCEKCRLVLCNPKQ--TECGHRFCESCMAALLSS 82
Db  358 REAENRLLEARSSIKEEQRYTLLDYRVTRGRSIVTNIRRVLSECRSK------------ 410

Qy   83 SSPKCTACQ--ESIIKDKVFKDNCCKREILALQYCR------------NEGRGCAEQLTLGHL 132
Db  411 EKPESVLERLDAVINDLESKARALDQEASALEAEAARRLVQALSMEESGGSARCPVCG-- 468

Qy  133 LVHLKNECQFEELPCLRADCCKEVLRKDLRDHVEKACKYREATCSHCKSQVPMIKLQKHE 192
Db  469 -------AELPPGRAEAIARYRHE-AERLRKAAKEKAAEAKARAEASRLQDKRRR 517

Qy  193 DTDCPCVVVSCPHKCSVQTLLR--SELSAHLSECVNAPSTCSFKRYGCVFQGTNQQIKAH 250
Db  518 ------------IELLLSRLNQLEEGLRE----------------LGFQTPEDLAKAE 547

Qy  251 EASSAV-QHVNLLKEWSNSLEKKVSLLQONESV---EKNKSIQSLHNQICSFEIEIEROK 305
Db  548 QKLRMLRERLEELRKLENSLEEKVRNLSREEVALREAKTRALEVLQR---LGIKEEAR 603

Qy  306 EMLRNNESKILHLQRVIDSQOAEKL-----------------------------KEL---DKE 335
Db  604 EKLKTLSSESKKLERMLVSKAEDLATRLGITTAYRSLDDLLEKAREALEGVDKELSALERR 663

Qy  336 IRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAGQAARNTGLLESQLSRHDQTLSVHD 395
Db  664 LEEARRLKEEAAKLKWEAEQVMKRLEELEAEEKKLRKEVSRKSEIEARLKEVQNTLAELD 723

Qy  396 IRLADMDLRFQVLEFASYNGVLIWKIRDYKRRKQEAVMGKTLSLY 440
Db  724 DRISRIDREMGELQT--------RIREMKSRK--ASGEEALKLY 757
```

RESULT 14
I49642
estrogen-responsive finger protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49642
R;Orimo, A.; Inoue, S.; Ikeda, K.; Noji, S.; Muramatsu, M.
J. Biol. Chem. 270, 24406-24413, 1995
A;Title: Molecular cloning, structure, and expression of mouse estrogen-responsive fi
A;Reference number: I49642; MUID:96025835; PMID:7592654
A;Accession: I49642
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-634 <RES>
A;Cross-references: GB:D63902; NID:g1088466; PIDN:BAA09941.1; PID:g1088467
C;Superfamily: RING finger homology
C;Keywords: zinc
F:9-59/Domain: RING finger homology <RNG>

Query Match   5.4%; Score 161; DB 2; Length 634;
Best Local Similarity 18.5%; Pred. No. 0.055;
Matches 75; Conservative 65; Mismatches 130; Indels 136; Gaps 17;

```
Qy   48 DRYKCEKCRLVLCNPKQTECGHRFCESCMAALLSSSSP--KCTACQESIIKDKVFKDNCC 105
Db    9 EELSCSVCLELFKEPVTTPCGHNFCTSCLDETWVVQGPPYRCPQCR-----KVYQ---V 59

Qy  106 KREILALQYVC----------RNEGRGCAEQLTLGHLLVHLK-NECQ 141
Db   60 RPQLQKNTVMCAVVEQFLQAEQARTPVDDWTPPARFSASSAATQVACDHCLTEIAVKTC- 118

Qy  142 FEELPCLRADCKEKV-------------LRKDLRDHVEKAC---KYREATCSHCKSQVP 184
Db  119 --LVCMASFCQEHLRPHFEDSPAFQDHPLQSPIRDLLRRKCTQHNRLREFFCP----- 168

Qy  185 MIKLQKHEDTDCPCVVVSCPHK-CSVQTLLRSELSAHLSECVNAPSTCSFKRYGCVFQGT 243
Db  169 -------EHGECICHICLVEHKTCSPTTL--SQASADL--------------------- 197

Qy  244 NQQIKAHEASSAVQHVNLLKEWSNSLEKKVSLLQONESVEKNKSIQSLHNQICSFEIEIER 303
Db  198 ------------------EYKLRNKLTIMHSHINGATKALEDVRSKQQCVQDSMKR 235

Qy  304 QKEMLRNNESKILHLQRVID----SQAEKLKELDKEI------RPFRQNWEEADSMKS 351
Db  236 KMEQLR---QEYMEMKAVIDAAETSSLRRLKEEEKRVYGKFDTIYQVLVKKKSEMQKLKA 292

Qy  352 SVESLQNRVTELESVDKSA---GOAARNTGLLESQLSRHDQTLSVH 394
Db  293 EVELIMDKGDEFEPLEKAAKLQGESTKPVYIPKIDLD-HDLIMGIY 337
```

RESULT 15
S18199
myosin heavy chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 02-Feb-2001
C;Accession: S18199
R;Stewart, A.F.R.; Camoretti-Mercado, B.; Perlman, D.; Gupta, M.; Jakovcic, S.; Zak,

```
Query Match          5.38;   Score 157.5; DB 2;   Length 1039;
Best Local Similarity   20.1%;   Pred. No. 0.16;   Indels 137;   Gaps   21;
Matches 102;  Conservative  85;  Mismatches 184;

Qy      14 QPNPPLKLQPDRGAGSVLVPEQQGGYKEKFVKTIVEDKYKCEKCRLVLCNPKQTECGHRFCE  73
           | : |: | ||||  ::|:|  |  : | | |  ||  :  || | | : |  ||  | :|
Db     528 QEDMMIDLEKANSAAASLDKKQRGF-DKIINDWKQKYEESQAEL-------EASQKEAR  578

Qy      74 SCMAALLSSSSPKCTACQQESIIKDKVFKDNCCKREILALQYYCRNEGRGCAEQLTLGHLL 133
           |  |  :   : |||  | :::||| :|: |: |  |:   ||||  || | | |||||
Db     579 SLSTELFKLKN---AYEETL--DHL---ETLKRENKNLQ---EEISDLTNQISEGNKN 625

Qy     134 VH-------------LKNEQFE------------------ELPCLRADCKEKVLRKD-- 160
           |:|                : | |     |:| |  | : ||
Db     626 LHEIEKVYKKQVEQEKSEVQLALEEAEGALEHEEESKTLRFQLELSQLKADFERKLAEKDEE 685

Qy     161 ---LRDHVEKACKYREATC-SHCKSQVPMIKLQKHEDTDCPCVVVSCPH----------- 205
              | | |  | ||  :|  :: |  | |  | | |  |  | |  |
Db     686 MQNIRRNQQRTIDSLQSTLDSEARSRNEAIRLKKKMEGDLNEMEIQLSHANRHAAEATKS 745

Qy     206 KCSVQTLLRSELS-----AHLSECVNAPSTCSFKRYGCVFQGTNQQIKA----------- 249
           :|| | | |||  :       :| |   :  | ||:|: |: |:
Db     746 ARGLQTQIK-ELQVQLDDLGHLNEDLKEQLAVSDRRNN-LLQSELDELRALLDQTERARK 803

Qy     250 ---HEASSAVQHVNLLKEWSNS---------LEKKVSLLQNESVEKNKSIQSLHNQICSFEI 299
              | |:| : | || ||:           |  | ::||:  : | | | || :| |
Db     804 LAEHELLEATERVNLLHTQNTSLINQKKLEGDISQMQNEVEESIQECRNAEQKAKKAIT 863

Qy     300 EIERQKEMLRNNESKILHLQRVTDSQAEKLKELDKEIRPFRQNWEEADSM-----KSSVE 354
           :| : | |:  |   | || |   :|: |||  |  | |  | :|  ||   :: ||:|
Db     864 DAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQKRL-------DEAEQIALKGGKKQIQ 916

Qy     355 SLQNRVTELES-----------VDKSAGQAARNTGLLESQLSRHDQTLSVHDIRLADMDL 403
           ||:|| || ::          |:| :| | || ::|: | |:::| | | |:|| |
Db     917 KLESRVRELENELENELRRNSDAQKGARKFERRIKELTYQSEEDKKNLA-----RMQDLID 972

Qy     404 RFQVLETASYNGVLIWKIRDYKRRKQEA 431
           : |:  || | :: ||  : :: ||
Db     973 KLQL--------KVKSYKHQAEEA 988

Search completed: December 19, 2002, 15:01:59
Job time : 25 secs
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